WHAT IS CLAIMED IS:

1.   A method for obtaining DNA fingerprint profile data, comprising the steps of:

     measuring peak intensity and size of each DNA fragment in a sample of genomic DNA;

     classifying the peak intensities of said fragments according to a predetermined discrete intensity level scale;

     aligning the sizes of said fragments into corresponding ones of discrete size bins;

     entering the classified peak intensities of said fragments into a data record in a sequence determined by said aligned sizes; and

     storing the record.

2.   The method of claim 1, wherein said sample is obtained by ALFP.

3.   The method of claim 1, wherein said sample is obtained by RLFP.

4.   The method of claim 1, wherein said sample is obtained by SSR PCR.

5.   The method of claim 1, wherein said sample is obtained by VNTR PCR.

6.   The method of claim 1, further comprising the step of normalizing the measured peak intensities of said fragments before classifying said peak intensities according to said discrete intensity level scale.

7.   The method of claim 6, wherein said discrete intensity level scale comprises at least five discrete peak levels.

8.   The method of claim 1, wherein the step of aligning comprises the steps of:

     grouping fragment sequences of said fragments into clusters, wherein adjacent peaks of each cluster are less

than or equal to a predetermined number of discrete positions apart;

assigning a potential energy value to each cluster, said potential energy value being proportional to the spacing between adjacent peaks of the cluster and to the amount of displacement required to bin the peaks into discrete size bins;

varying the displacement of said peaks so that said potential energy value is minimized; and

aligning said peaks into discrete size bins according to the displacement values that result in a minimized potential energy value.

9.   The method of claim 1, wherein said step of entering comprises the step of creating a data record having:
an information field including

an identification of the source of the genomic DNA,

the method of producing DNA fragments from said source,

the spacing between successive fragments,

the starting size of said fragments, and

the ending size of said fragments; and

a sequence field containing a sequence of said classified peak intensities.

10.   The method of claim 9, further comprising the step of scoring a comparison between two data records, including the steps of assigning reward points to matches of peak intensities and penalty points to mismatches of peak intensities, based on the relative magnitude of said peak intensities, comparing said two data records for identical matches at corresponding size positions, comparing said two data records for identical matches at adjacent size positions, comparing said two data records for non-

identical matches at corresponding size positions, and comparing said two data records for non-identical matches at adjacent size positions, and totaling said reward points and penalty points according to found matches and remaining mismatches to obtain a score.

11. The method of claim 10, further comprising the step of obtaining a percentage metric for two compared data records, by obtaining a ratio of said score to a score obtained by matching one of said two data records to itself.

12. A computer program product, comprising:

a computer-readable medium having computer-executable code recorded thereon for obtaining DNA fingerprint profile data, said computer-executable code comprising:

means for measuring peak intensity and size of each DNA fragment in a sample of genomic DNA;

means for classifying the peak intensities of said fragments according to a predetermined discrete intensity level scale;

means for aligning the sizes of said fragments into corresponding ones of discrete size bins;

means for entering the classified peak intensities of said fragments into a data record in a sequence determined by said aligned sizes; and

means storing the record in a computer-readable storage medium.

13. The computer program product of claim 12, further comprising:

means for normalizing the measured peak intensities of said fragments before classifying said peak intensities according to said discrete intensity level scale.
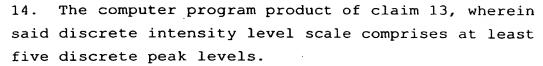
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14. The computer program product of claim 13, wherein said discrete intensity level scale comprises at least five discrete peak levels.

15. The computer program product of claim 12, wherein said means for aligning comprises:

means for grouping fragment sequences of said fragments into clusters, wherein adjacent peaks of each

5   cluster are less than or equal to a predetermined number of discrete positions apart;

means for assigning a potential energy value to each cluster, said potential energy value being proportional to the spacing between adjacent peaks of the cluster and to

10   the amount of displacement required to bin the peaks into discrete size bins;

means for varying the displacement of said peaks so that said potential energy value is minimized; and

means for aligning said peaks into discrete size bins

15   according to the displacement values that result in a minimized potential energy value.

16. The computer program product of claim 12, wherein said means for entering comprises means for creating a data record having:

an information field including

5   an identification of the source of the genomic DNA,

the method of producing DNA fragments from said source,

the spacing between successive fragments,

the starting size of said fragments, and

10   the ending size of said fragments; and

a sequence field containing a sequence of said classified peak intensities.

17.   A DNA fingerprint data record stored in a computer-
readable storage medium, said DNA fingerprint data
including size and peak intensity of DNA fragments
produced from a DNA sample obtained from a source of
5   genomic DNA, said data record comprising:
an information field including
        an identification of said source of genomic DNA,
        the method of producing DNA fragments from said
source,
10   the spacing between successive fragments,
        the starting size of said fragments, and
        the ending size of said fragments; and
a sequence field containing a sequence of classified peak
intensities.